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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,795

DATE: 05/20/2002

TIME: 11:48:42

Input Set : A:\09931795.txt

Output Set: N:\CRF3\05202002\I931795.raw

ENTERED

4 <110> APPLICANT: ROZEN, Rima
7 <120> TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
8 REDUCTASE AND USES THEREOF
11 <130> FILE REFERENCE: 04844/005003
13 <140> CURRENT APPLICATION NUMBER: 09/931,795
14 <141> CURRENT FILING DATE: 2001-08-16
16 <150> PRIOR APPLICATION NUMBER: US 09/592,595
17 <151> PRIOR FILING DATE: 2000-06-12
19 <150> PRIOR APPLICATION NUMBER: US 09/258,928
20 <151> PRIOR FILING DATE: 1999-03-01
22 <150> PRIOR APPLICATION NUMBER: US 08/738,000
23 <151> PRIOR FILING DATE: 1997-02-12
25 <150> PRIOR APPLICATION NUMBER: PCT/CA95/00314
26 <151> PRIOR FILING DATE: 1995-05-25
28 <150> PRIOR APPLICATION NUMBER: GB 9410620.0
29 <151> PRIOR FILING DATE: 1994-05-26
31 <160> NUMBER OF SEQ ID NOS: 18
33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 2220
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)...(1980)
44 <400> SEQUENCE: 1
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46 Asn Ser Gly Ala Met Val Asn Glu Ala Arg Gly Asn Ser Ser Leu Asn
47 1 5 10 15
49 ccc tgc ttg gag ggc agt gcc agc agt ggc agt gag agc tcc aaa gat 96
50 Pro Cys Leu Glu Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp
51 20 25 30
53 agt tcg aga tgt tcc acc ccg ggc ctg gac cct gag cgg cat gag aga 144
54 Ser Ser Arg Cys Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg
55 35 40 45
57 ctc cgg gag aag atg agg cgg cga ttg gaa tct ggt gac aag tgg ttc 192
58 Leu Arg Glu Lys Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe
59 50 55 60
61 tcc ctg gaa ttc ttc cct cct cga act gct gag gga gct gtc aat ctc 240
62 Ser Leu Glu Phe Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu
63 65 70 75 80
65 atc tca agg ttt gac cgg atg gca gca ggt ggc ccc ctc tac ata gac 288
66 Ile Ser Arg Phe Asp Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp

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133	tgg	gct	ctc	agt	gcc	cac	ccc	aag	cgc	cga	gag	gaa	gat	gta	cgt	ccc	1104
134	Trp	Ala	Leu	Ser	Ala	His	Pro	Lys	Arg	Arg	Glu	Glu	Asp	Val	Arg	Pro	
135			355					360					365				
137	atc	ttc	tgg	gcc	tcc	aga	cca	aag	agt	tac	atc	tac	cgt	acc	cag	gag	1152
138	Ile	Phe	Trp	Ala	Ser	Arg	Pro	Lys	Ser	Tyr	Ile	Tyr	Arg	Thr	Gln	Glu	
139		370					375					380					
141	tgg	gac	gag	ttc	cct	aac	ggc	cgc	tgg	ggc	aat	tcc	tct	tcc	cct	gcc	1200
142	Trp	Asp	Glu	Phe	Pro	Asn	Gly	Arg	Trp	Gly	Asn	Ser	Ser	Ser	Pro	Ala	
143	385					390					395					400	
145	ttt	ggg	gag	ctg	aag	gac	tac	tac	ctc	ttc	tac	ctg	aag	agc	aag	tcc	1248
146	Phe	Gly	Glu	Leu	Lys	Asp	Tyr	Tyr	Leu	Phe	Tyr	Leu	Lys	Ser	Lys	Ser	
147					405					410					415		
149	ccc	aag	gag	gag	ctg	ctg	aag	atg	tgg	ggg	gag	gag	ctg	acc	agt	gaa	1296
150	Pro	Lys	Glu	Glu	Leu	Leu	Lys	Met	Trp	Gly	Glu	Glu	Leu	Thr	Ser	Glu	
151				420						425					430		
153	gca	agt	gtc	ttt	gaa	gtc	ttt	gtt	ctt	tac	ctc	tcg	gga	gaa	cca	aac	1344
154	Ala	Ser	Val	Phe	Glu	Val	Phe	Val	Leu	Tyr	Leu	Ser	Gly	Glu	Pro	Asn	
155			435					440					445				
157	cgg	aat	ggt	cac	aaa	gtg	act	tgc	ctg	ccc	tgg	aac	gat	gag	ccc	ctg	1392
158	Arg	Asn	Gly	His	Lys	Val	Thr	Cys	Leu	Pro	Trp	Asn	Asp	Glu	Pro	Leu	
159		450					455					460					
161	gcg	gct	gag	acc	agc	ctg	ctg	aag	gag	gag	ctg	ctg	cgg	gtg	aac	cgc	1440
162	Ala	Ala	Glu	Thr	Ser	Leu	Leu	Lys	Glu	Glu	Leu	Leu	Arg	Val	Asn	Arg	
163	465					470					475					480	
165	cag	ggc	atc	ctc	acc	atc	aac	tca	cag	ccc	aac	atc	aac	ggg	aag	ccg	1488
166	Gln	Gly	Ile	Leu	Thr	Ile	Asn	Ser	Gln	Pro	Asn	Ile	Asn	Gly	Lys	Pro	
167					485					490					495		
169	tcc	tcc	gac	ccc	atc	gtg	ggc	tgg	ggc	ccc	agc	ggg	ggc	tat	gtc	ttc	1536
170	Ser	Ser	Asp	Pro	Ile	Val	Gly	Trp	Gly	Pro	Ser	Gly	Gly	Tyr	Val	Phe	
171				500						505				510			
173	cag	aag	gcc	tac	tta	gag	ttt	ttc	act	tcc	cgc	gag	aca	gcg	gaa	gca	1584
174	Gln	Lys	Ala	Tyr	Leu	Glu	Phe	Phe	Thr	Ser	Arg	Glu	Thr	Ala	Glu	Ala	
175			515					520					525				
177	ctt	ctg	caa	gtg	ctg	aag	aag	tac	gag	ctc	cgg	gtt	aat	tac	cac	ctt	1632
178	Leu	Leu	Gln	Val	Leu	Lys	Lys	Tyr	Glu	Leu	Arg	Val	Asn	Tyr	His	Leu	
179		530					535					540					
181	gtc	aat	gtg	aag	ggt	gaa	aac	atc	acc	aat	gcc	cct	gaa	ctg	cag	ccg	1680
182	Val	Asn	Val	Lys	Gly	Glu	Asn	Ile	Thr	Asn	Ala	Pro	Glu	Leu	Gln	Pro	
183	545					550					555					560	
185	aat	gct	gtc	act	tgg	ggc	atc	ttc	cct	ggg	cga	gag	atc	atc	cag	ccc	1728
186	Asn	Ala	Val	Thr	Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Ile	Gln	Pro	
187					565					570					575		
189	acc	gta	gtg	gat	ccc	gtc	agc	ttc	atg	ttc	tgg	aag	gac	gag	gcc	ttt	1776
190	Thr	Val	Val	Asp	Pro	Val	Ser	Phe	Met	Phe	Trp	Lys	Asp	Glu	Ala	Phe	
191				580						585					590		
193	gcc	ctg	tgg	att	gag	cgg	tgg	gga	aag	ctg	tat	gag	gag	gag	tcc	ccg	1824
194	Ala	Leu	Trp	Ile	Glu	Arg	Trp	Gly	Lys	Leu	Tyr	Glu	Glu	Glu	Ser	Pro	
195			595					600							605		
197	tcc	cgc	acc	atc	atc	cag	tac	atc	cac	gac	aac	tac	ttc	ctg	gtc	aac	1872

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198 Ser Arg Thr Ile Ile Gln Tyr Ile His Asp Asn Tyr Phe Leu Val Asn
199      610      615      620
201 ctg gtg gac aat gac ttc cca ctg gac aac tgc ctc tgg cag gtg gtg      1920
202 Leu Val Asp Asn Asp Phe Pro Leu Asp Asn Cys Leu Trp Gln Val Val
203 625      630      635      640
205 gaa gac aca ttg gag ctt ctc aac agg ccc acc cag aat gcg aga gaa      1968
206 Glu Asp Thr Leu Glu Leu Leu Asn Arg Pro Thr Gln Asn Ala Arg Glu
207      645      650      655
209 acg gag gct cca tgacctgag tctgacgcc ctgcgttgga gccactcctg      2020
210 Thr Glu Ala Pro
211      660
213 tcccgcccttc ctctccaca gtgctgcttc tcttggaac tccactctcc ttcgtgtctc      2080
214 tcccaccccg gcctccactc cccacctga caatggcagc tagactggag tgaggcttcc      2140
215 aggtcttctc tggacctgag tcggccccac atgggaacct agtactctct gctctaaaaa      2200
216 aaaaaaaaaa aaaggaattc      2220
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219 <211> LENGTH: 660
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 2
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225 1      5      10      15
226 Pro Cys Leu Glu Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp
227      20      25      30
228 Ser Ser Arg Cys Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg
229      35      40      45
230 Leu Arg Glu Lys Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe
231      50      55      60
232 Ser Leu Glu Phe Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu
233 65      70      75      80
234 Ile Ser Arg Phe Asp Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp
235      85      90      95
236 Val Thr Trp His Pro Ala Gly Asp Pro Gly Ser Asp Lys Glu Thr Ser
237      100      105      110
238 Ser Met Met Ile Ala Ser Thr Ala Val Asn Tyr Cys Gly Leu Glu Thr
239      115      120      125
240 Ile Leu His Met Thr Cys Cys Arg Gln Arg Leu Glu Glu Ile Thr Gly
241      130      135      140
242 His Leu His Lys Ala Lys Gln Leu Gly Leu Lys Asn Ile Met Ala Leu
243 145      150      155      160
244 Arg Gly Asp Pro Ile Gly Asp Gln Trp Glu Glu Glu Glu Gly Gly Phe
245      165      170      175
246 Asn Tyr Ala Val Asp Leu Val Lys His Ile Arg Ser Glu Phe Gly Asp
247      180      185      190
248 Tyr Phe Asp Ile Cys Val Ala Gly Tyr Pro Lys Gly His Pro Glu Ala
249      195      200      205
250 Gly Ser Phe Glu Ala Asp Leu Lys His Leu Lys Glu Lys Val Ser Ala
251      210      215      220
252 Gly Ala Asp Phe Ile Ile Thr Gln Leu Phe Phe Glu Ala Asp Thr Phe

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253 225                230                235                240
254 Phe Arg Phe Val Lys Ala Cys Thr Asp Met Gly Ile Thr Cys Pro Ile
255                245                250                255
256 Val Pro Gly Ile Phe Pro Ile Gln Gly Tyr His Ser Leu Arg Gln Leu
257                260                265                270
258 Val Lys Leu Ser Lys Leu Glu Val Pro Gln Glu Ile Lys Asp Val Ile
259                275                280                285
260 Glu Pro Ile Lys Asp Asn Asp Ala Ala Ile Arg Asn Tyr Gly Ile Glu
261                290                295                300
262 Leu Ala Val Ser Leu Cys Gln Glu Leu Leu Ala Ser Gly Leu Val Pro
263 305                310                315                320
264 Gly Leu His Phe Tyr Thr Leu Asn Arg Glu Met Ala Thr Thr Glu Val
265                325                330                335
266 Leu Lys Arg Leu Gly Met Trp Thr Glu Asp Pro Arg Arg Pro Leu Pro
267                340                345                350
268 Trp Ala Leu Ser Ala His Pro Lys Arg Arg Glu Glu Asp Val Arg Pro
269                355                360                365
270 Ile Phe Trp Ala Ser Arg Pro Lys Ser Tyr Ile Tyr Arg Thr Gln Glu
271                370                375                380
272 Trp Asp Glu Phe Pro Asn Gly Arg Trp Gly Asn Ser Ser Ser Pro Ala
273 385                390                395                400
274 Phe Gly Glu Leu Lys Asp Tyr Tyr Leu Phe Tyr Leu Lys Ser Lys Ser
275                405                410                415
276 Pro Lys Glu Glu Leu Leu Lys Met Trp Gly Glu Glu Leu Thr Ser Glu
277                420                425                430
278 Ala Ser Val Phe Glu Val Phe Val Leu Tyr Leu Ser Gly Glu Pro Asn
279                435                440                445
280 Arg Asn Gly His Lys Val Thr Cys Leu Pro Trp Asn Asp Glu Pro Leu
281                450                455                460
282 Ala Ala Glu Thr Ser Leu Leu Lys Glu Glu Leu Leu Arg Val Asn Arg
283 465                470                475                480
284 Gln Gly Ile Leu Thr Ile Asn Ser Gln Pro Asn Ile Asn Gly Lys Pro
285                485                490                495
286 Ser Ser Asp Pro Ile Val Gly Trp Gly Pro Ser Gly Gly Tyr Val Phe
287                500                505                510
288 Gln Lys Ala Tyr Leu Glu Phe Phe Thr Ser Arg Glu Thr Ala Glu Ala
289                515                520                525
290 Leu Leu Gln Val Leu Lys Lys Tyr Glu Leu Arg Val Asn Tyr His Leu
291                530                535                540
292 Val Asn Val Lys Gly Glu Asn Ile Thr Asn Ala Pro Glu Leu Gln Pro
293 545                550                555                560
294 Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Ile Gln Pro
295                565                570                575
296 Thr Val Val Asp Pro Val Ser Phe Met Phe Trp Lys Asp Glu Ala Phe
297                580                585                590
298 Ala Leu Trp Ile Glu Arg Trp Gly Lys Leu Tyr Glu Glu Glu Ser Pro
299                595                600                605
300 Ser Arg Thr Ile Ile Gln Tyr Ile His Asp Asn Tyr Phe Leu Val Asn
301                610                615                620

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/931,795

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TIME: 11:48:43

Input Set : A:\09931795.txt

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Creation date: 27-03-2003
Indexing Officer: EGEDLU - ESKINDER GEDLU
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No.	Doccode	Number of pages
1	IDS	2

Total number of pages: 2

Remarks:

Order of re-scan issued on